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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/062,879
 DATE: 05/07/2002
 TIME: 11:33:41

Input Set : N:\Crf3\RULE60\10062879.raw
 Output Set: N:\CRF3\05072002\J062879.raw

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1 <110> APPLICANT: Cockett, Mark I.
2     Dिल्s, Daniel W.
3     Chang Ling, Huai-Ping
4     Sokol, Patricia T.
5 <120> TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
6     Polypeptides and Uses Therefor
7 <130> FILE REFERENCE: ahp-98089
8 <140> CURRENT APPLICATION NUMBER: 10/062,879
9 <141> CURRENT FILING DATE: 2002-01-31
11 <150> PRIOR APPLICATION NUMBER: US/09/178,109
12 <151> PRIOR FILING DATE: 1998-10-23
15 <160> NUMBER OF SEQ ID NOS: 4
16 <170> SOFTWARE: PatentIn Ver. 2.0
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20 <212> TYPE: DNA
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25     atcggttgga tgccggtggc caactgcccc atgccctgg ccccgccga caagaacaag 180
26     cggcaggatg agctgattgt cctcaacgtg agtgggcgga ggttccagac cttgaggacc 240
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28     gagcacacca aggagttactt cttcgaccgg gaccocgagg tgttccggt cgtgtctaac 360
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30     gagctggcct tctacggcat cctccggag atcatcgggg actgctgcta cgaggagta 480
31     aaggaccyga agagggagaa cgccgagcgg ctcattgacg acaacgactc ggagaacaac 540
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34     gtcatcacca acgtggtgga gacggtgccg tgcggcacgg tcccgggcag caaggagctg 720
35     ccgtgcgggg agcgctactc ggtggccttc ttctgcctgg acacggcggt cgtcatgac 780
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46     aggtcgaatg catcactgca cagcaagcgc aacgggctcc tcacagcagg cctggagctg 1440
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48 catcacctgc tgcactgcct ggaaaaaac aactgggttgt cctatttgt ggatgatccc 1560
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52 ctgcaccaatt ctaacctgcc agctactcgc ctgcgcagca tgcaagagct cagcagcgtc 1800
53 cacatccagg gcagtgcagc gccctccctc acaaccagtc gctccagcct taatttgaaa 1860
54 gcagacgacg gactgcagcc aaactgcmaa acatcccaga tcaccacagc catcatcagc 1920
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69 Asp Lys Asn Lys Arg Gln Asp Glu Leu Ile Val Leu Asn Val Ser Gly
70 35 40 45
71 Arg Arg Phe Gln Thr Trp Arg Thr Leu Glu Arg Tyr Pro Asp Thr
72 50 55 60
73 Leu Leu Gly Ser Thr Glu Lys Glu Phe Phe Phe Asn Glu Asp Thr Lys
74 65 70 75 80
75 Glu Tyr Phe Phe Asp Arg Asp Pro Glu Val Phe Arg Cys Val Leu Asn
76 85 90 95
77 Phe Tyr Arg Thr Gly Lys Leu His Tyr Pro Arg Tyr Glu Cys Ile Ser
78 100 105 110
79 Ala Tyr Asp Asp Glu Leu Ala Phe Tyr Gly Ile Leu Pro Glu Ile Ile
80 115 120 125
81 Gly Asp Cys Cys Tyr Glu Glu Tyr Lys Asp Arg Lys Arg Glu Asn Ala
82 130 135 140
83 Glu Arg Leu Met Asp Asp Asn Asp Ser Glu Asn Asn Gln Glu Ser Met
84 145 150 155 160
85 Pro Ser Leu Ser Phe Arg Gln Thr Met Trp Arg Ala Phe Glu Asn Pro
86 165 170 175
87 His Thr Ser Thr Leu Ala Leu Val Phe Tyr Tyr Val Thr Gly Phe Phe
88 180 185 190
89 Ile Ala Val Ser Val Ile Thr Asn Val Val Glu Thr Val Pro Cys Gly
90 195 200 205
91 Thr Val Pro Gly Ser Lys Glu Leu Pro Cys Gly Glu Arg Tyr Ser Val
92 210 215 220
93 Ala Phe Phe Cys Leu Asp Thr Ala Cys Val Met Ile Phe Thr Val Glu
94 225 230 235 240
95 Tyr Leu Leu Arg Leu Phe Ala Ala Pro Ser Arg Tyr Arg Phe Ile Arg
96 245 250 255
97 Ser Val Met Ser Ile Ile Asp Val Val Ala Ile Met Pro Tyr Tyr Ile

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103 Gln Gly Leu Arg Ile Leu Gly Tyr Thr Leu Lys Ser Cys Ala Ser Glu
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105 Leu Gly Phe Leu Leu Phe Ser Leu Thr Met Ala Ile Ile Ile Phe Ala
106          325          330          335
107 Thr Val Met Phe Tyr Ala Glu Lys Gly Ser Ser Ala Ser Lys Phe Thr
108          340          345          350
109 Ser Ile Pro Ala Ser Phe Trp Tyr Thr Ile Val Thr Met Thr Thr Leu
110          355          360          365
111 Gly Tyr Gly Asp Met Val Pro Lys Thr Ile Ala Gly Lys Ile Phe Gly
112          370          375          380
113 Ser Ile Cys Ser Leu Ser Gly Val Leu Val Ile Ala Leu Pro Val Pro
114          385          390          395          400
115 Val Ile Val Ser Asn Phe Ser Arg Ile Tyr His Gln Asn Gln Arg Ala
116          405          410          415
117 Asp Lys Arg Arg Ala Gln Lys Lys Ala Arg Leu Ala Arg Ile Arg Val
118          420          425          430
119 Ala Lys Thr Gly Ser Ser Asn Ala Tyr Leu His Ser Lys Arg Asn Gly
120          435          440          445
121 Leu Leu Asn Glu Ala Leu Glu Leu Thr Gly Thr Pro Glu Glu Glu His
122          450          455          460
123 Met Gly Lys Thr Thr Ser Leu Ile Glu Ser Gln His His His Leu Leu
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125 His Cys Leu Glu Lys Thr Thr Gly Leu Ser Tyr Leu Val Asp Asp Pro
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128          500          505          510
129 Glu Gln Met Phe Glu Gln Asn Cys Met Glu Ser Ser Met Gln Asn Tyr
130          515          520          525
131 Pro Ser Thr Arg Ser Pro Ser Leu Ser Ser His Pro Gly Leu Thr Thr
132          530          535          540
133 Thr Cys Cys Ser Arg Arg Ser Lys Lys Thr Thr His Leu Pro Asn Ser
134          545          550          555          560
135 Asn Leu Pro Ala Thr Arg Leu Arg Ser Met Gln Glu Leu Ser Thr Ile
136          565          570          575
137 His Ile Gln Gly Ser Glu Gln Pro Ser Leu Thr Thr Ser Arg Ser Ser
138          580          585          590
139 Leu Asn Leu Lys Ala Asp Asp Gly Leu Arg Pro Asn Cys Lys Thr Ser
140          595          600          605
141 Gln Ile Thr Thr Ala Ile Ile Ser Ile Pro Thr Pro Pro Ala Leu Thr
142          610          615          620
143 Pro Glu Gly Glu Ser Arg Pro Pro Pro Ala Ser Pro Gly Pro Asn Thr
144          625          630          635          640
145 Asn Ile Pro Ser Ile Thr Ser Asn Val Val Lys Val Ser Val Leu
146          645          650          655

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155 atcgggtgga tgcgggtggc caactgcccc atgccccctg ccccgccgga caagaacaag 180
156 cggcaggatg agctgattgt cctcaacgtg agtgggcgga ggttccagac ctggaggacc 240
157 acgtggagtc gctacccgga caccctgctg ggcagcagg aaaggagatt cttcttcaac 300
158 gaggacacca aggagtactt cttcgaccgg gaccccgagg tcttcgcgtg cgtgctcaac 360
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162 caggagtcca tgccttcgct cagcttccgc cagaccatgt ggcgggcctt cgagaacccc 600
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164 gtcacacca acgtggtgga gacggtgcgg tgcggcagg tcccgggcag caaggagctg 720
165 ccgtgcyggy agcgtactct ggtggccttc tctgctctgg acacggcggt cgtcatgctc 780
166 ttacacgtgg agtacctctc ggcgctcttc gcggctccca ccgcctacgg ctctcatccg 840
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168 accaacaacg aggacgtgtc cggcgctctc gtcacgtctc ggtcttcagg gctctcagg 960
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191 <212> TYPE: PRT
192 <213> ORGANISM: human
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197 20 25 30

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198 Asp Lys Asn Lys Arg Gln Asp Glu Leu Ile Val Leu Asn Val Ser Gly
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201           50           55           60
202 Leu Leu Gly Ser Thr Glu Lys Glu Phe Phe Phe Asn Glu Asp Thr Lys
203           65           70           75           80
204 Glu Tyr Phe Phe Asp Arg Asp Pro Glu Val Phe Arg Cys Val Leu Asn
205           85           90           95
206 Phe Tyr Arg Thr Gly Lys Leu His Tyr Pro Arg Tyr Glu Cys Ile Ser
207           100          105          110
208 Ala Tyr Asp Asp Glu Leu Ala Phe Tyr Gly Ile Leu Pro Glu Ile Ile
209           115          120          125
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211           130          135          140
212 Glu Arg Leu Met Asp Asp Asn Asp Ser Glu Asn Asn Gln Glu Ser Met
213           145          150          155          160
214 Pro Ser Leu Ser Phe Arg Gln Thr Met Trp Arg Ala Phe Glu Asn Pro
215           165          170          175
216 His Thr Ser Thr Leu Ala Leu Val Phe Tyr Tyr Val Thr Gly Phe Phe
217           180          185          190
218 Ile Ala Val Ser Val Ile Thr Asn Val Val Glu Thr Val Pro Cys Gly
219           195          200          205
220 Thr Val Pro Gly Ser Lys Glu Leu Pro Cys Gly Glu Arg Tyr Ser Val
221           210          215          220
222 Ala Phe Phe Cys Leu Asp Thr Ala Cys Val Met Ile Phe Thr Val Glu
223           225          230          235          240
224 Tyr Leu Leu Arg Leu Phe Ala Ala Pro Ser Arg Tyr Arg Phe Ile Arg
225           245          250          255
226 Ser Val Met Ser Ile Ile Asp Val Val Ala Ile Met Pro Tyr Tyr Ile
227           260          265          270
228 Gly Leu Val Met Thr Asn Asn Glu Asp Val Ser Gly Ala Phe Val Thr
229           275          280          285
230 Leu Arg Val Phe Arg Val Phe Arg Ile Phe Lys Phe Ser Arg His Ser
231           290          295          300
232 Gln Gly Leu Arg Ile Leu Gly Tyr Thr Leu Lys Ser Cys Ala Ser Glu
233           305          310          315          320
234 Leu Gly Phe Leu Leu Phe Ser Leu Thr Met Ala Ile Ile Ile Phe Ala
235           325          330          335
236 Thr Val Met Phe Tyr Ala Glu Lys Gly Ser Ser Ala Ser Lys Phe Thr
237           340          345          350
238 Ser Ile Pro Ala Ser Phe Trp Tyr Thr Ile Val Thr Met Thr Thr Leu
239           355          360          365
240 Gly Tyr Gly Asp Met Val Pro Lys Thr Ile Ala Gly Lys Ile Phe Gly
241           370          375          380
242 Ser Ile Cys Ser Leu Ser Gly Val Leu Val Ile Ala Leu Pro Val Pro
243           385          390          395          400
244 Val Ile Val Ser Asn Phe Ser Arg Ile Tyr His Gln Asn Gln Arg Ala
245           405          410          415
246 Asp Lys Arg Arg Ala Gln Lys Lys Ala Arg Leu Ala Arg Ile Arg Val

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VERIFICATION SUMMARY

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